

```

momp
incC
pomp91a      MKQMRLWGFLFLSSFCQVSYLRANDVLLFLSGIHSGEDLELFTLRSSSPKTKTYSIAKDF

momp
incC
pomp91a      -----MKKLLKSVLVFAALSSASSLQALPVG-----
-----MTSPIPFQ-----
IVCDFAGNSIHKPGAFLNLKGDLEFFINSTPLAALTFKNIHLGARGAGLFSESNVTFKGL
. : .

momp
incC
pomp91a      -----NPAEPSIMIDGILWEGFGGDFCDPCATWCDALSMRVGGYGVDFV
-----SSGDASFLAEQPQLPSTSESQVLTQLLTMMKHQALSETVLQQ
HSLVLENNESWGGVLTTSBGDLSFINNTSVLCQNNISYGPGGALLLQGRKSKALFFDRNRG
. . . : * : : . : .

momp
incC
pomp91a      DRVLKTDVNKEFQMGAKFTTDTGNSAAPS-----
QRDRLEPTASIIILQVGGAFTGGAGAPFQG-----
TILFLKNKAVNQDESHPGYGGAVSSISPGSPITFADNQEILFQENEGELGGAIYNDQGA
. . . : . * .

momp
incC
pomp91a      -----TLTARENPAFYGRHMQDAEMFTNAACMALNIWDR-----
-----PADDHHPHPIPPFVVPAQIETEITIRSELQIMR-----
TFENNFTQTSFFSNKASFEELSIAATAISIHSGAIPYSLKTLLOKLGGAHADVHIRDC
. . . : : : *

momp
incC
pomp91a      --FDVFCTLGATSGYLKGNASFNVLVGLFGDNENQKTVKAESVPNMSFDQSVVELYTDTT
--STLQQSTKGARTGVLVVTAIIMTISLLAIIIIILAVLGFTG--VLPQVALLMQGETN
KGSIVFEENSATAGGAIAVNAVCNINAQGPVRFINNSALGLNGGAIYMQATGSILRLHAN
. : . : * . . . : : .

momp
incC
pomp91a      -----FAWSVGARAALWECGCATLG-----
-----LIWAMVSGSIICFIALIG-----
QGDIEFCGNKVRSSQFHSINSTSNFTNNAITIQAGPREFSLSANEGHRICFYDPIISATE
. . . * .

momp
incC
pomp91a      -----
-----
NYNLSLYINHQRLLLEAGGAVIFSGARLSPEHKKENKNKTSIINQPVRLCSGVLSIEGGAIL

momp
incC
pomp91a      -----ASFOYAQSKPKVEELNVLNAAEF
-----TLGLILTNKNTPLEAS
AVRSFYQEGGLLALGPGSKLTTQGNSEKDKIVITNLGFNLNLDSSDPAEIRATEKASI
. : . : .

momp
incC
pomp91a      TINKPKGYVGKEFFDLDTAGTDAATG-----
EISGVPRVYGHTESFYENHEYASKPYTTSIILSAKKLVTAAPSREPKDIONLIIAESEYMG

momp
incC
pomp91a      -----TKOASIDYHEWQASLALSRYLRNMFPTYIGVKWSRASFDADTIRIA
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YGYQGSWEFSWSPNDTKEKKTIIASWTPTEGFSLDPKRRGSEIPTTLWSTFSGLNIASNI

momp
incC
pomp91a      QPKSATAIFDTTTTLNPTIAGAGDVKTGAEGQLGDTMQIVSLQLNKMKSRSKSCGIAVGTTI

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pomp91a      VNNNYLNNSEVIPLQHLCVFGGPVYQIMEQNPKQSSNNLLVQHAGHNVGARIFFSFNTIL
momp         VDADKYAVTVETRLIDERAHVNAQFRF-----
incC         -----
pomp91a      SAALTQLFSSSSQQNVADKSHAQILIGTVSLNKSQALSLRSSFSYTEDSQVMKHVFPYK
momp         -----
incC         -----
pomp91a      GTSRGSWARNYGWGSVGMSSYAYPKGIRYLKMTFFVDLQYTKLVQNPFEVETGYDPRYFSSS
momp         -----
incC         -----
pomp91a      EMTNLSLPIGIALEMRFIGSRSSSLFLOVSTSYIKDLRRVNPQSSASLVLNHYTWDIQGVF
momp         -----
incC         -----
pomp91a      LGKEALNITLNSTIKYKIVTAYMGISSTQREGSNLSANAHAGLSLSF
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“*” means that the residues or nucleotides in that column are identical in all sequences in the alignment

“.” means that conserved substitutions have been observed

“:” means that semi-conserved substitutions are observed

6693087pomp91a seq
947 aa linear PAT 20-FEB-2004

LOCUS AAS37561
DEFINITION Sequence 3 from patent US 6693087.
ACCESSION AAS37561
VERSION AAS37561.1 GI:42715796
DBSOURCE accession AAS37561.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (residues 1 to 947)
AUTHORS Murdin,A.D., Dunn,P.L. and Oomen,R.P.
TITLE Nucleic acid molecules encoding POMP91A protein of Chlamydia
JOURNAL Patent: US 6693087-A 3 17-FEB-2004;
Aventis Pasteur Limited; Toronto;
CAX;
REMARK CAMBIA Patent Lens: US 6693087
FEATURES Location/Qualifiers
source 1..947
/organism="unknown"

ORIGIN

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121	hslvlennes	wggvlttsgd	lsfinntsvl	cqnnisyggg	ga11lqgrks	kalffrdnrg
181	tilflknkav	nqdeshpqyg	gavssispgs	pitfadnqei	lfqenegelg	gaiyndggai
241	tfennfqttt	ffsnkasfee	lsiaataisi	hsgaipyslk	tllqklggai	hadyvhirdc
301	kgsivfeens	ataggaiavn	avcdinaqgp	vrfinnsalg	lnggaiymqa	tgsilrlhan
361	qgdiefcgkn	vrsqfhshin	stsnftnnai	tiqqaprefs	lsaneghric	fydpiisate
421	nynslyinhq	rlleaggavi	fsgarlspah	kkenknktsi	inqpvrclsg	vl sieggail
481	avrsfyqegg	llalpggskl	ttqgknsekd	kivitnlgn	lenldssdpa	eiratekasi
541	eisgvprvyg	htesfyenhe	yaskpyttsi	ilsakklvta	psrpekdiqn	liiaeesymg
601	ygyqgswefts	wspndtkekk	tiiaswtptg	efsl dpkrrg	sfipttlwst	fsglniasni
661	vnnnylnnse	viplqhlcvf	ggpvyqimeq	npkqssnnll	vqhaghnvga	ripfsntil
721	saaltqlfss	ssqgnvadks	haqiligtvs	lnkswqalsl	rssfsyteds	qvmkhvfpyk
781	gtsrgswrny	gwsqsvqmsy	aypkqirylk	mtpfvdlyqt	klvqnpfvet	gydptryfss
841	emtnlslpig	ialemrfigs	rsslflqvst	syikdlrrvn	pqssaslvln	hytwdiqgvv
901	lgkealniti	nstikyki	aymgisstqr	egsnlsanah	aglsisf	

6686339incc seq
203 aa linear PAT 20-FEB-2004

LOCUS AAS33023
DEFINITION Sequence 3 from patent US 6686339.
ACCESSION AAS33023
VERSION AAS33023.1 GI:42707452
DBSOURCE accession AAS33023.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (residues 1 to 203)
AUTHORS Murdin,A.D., Dunn,P.L. and Oomen,R.P.
TITLE Nucleic acid molecules encoding inclusion membrane protein C of
Chlamydia
JOURNAL Patent: US 6686339-A 3 03-FEB-2004;
Aventis Pasteur Limited; Toronto;
CAX;
REMARK CAMBIA Patent Lens: US 6686339
FEATURES Location/Qualifiers
source 1..203
/organism="unknown"

ORIGIN
1 mtspipfqss gdsflaeqp qqlpstsesq lvtqlltmmk htgalsetvl qqrdrllpta
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121 tkgartgvlv vtailmtisl laiiilav lgftgvlpqv allmqgetnl iwamvsgsll
181 cfialigtlg liltknkntpl pas

LOCUS Q46409 *stephens momp* 393 aa linear BCT 02-MAY-2006
 DEFINITION Major outer membrane protein, serovar D precursor (MOMP).
 ACCESSION Q46409
 VERSION Q46409 GI:6707730
 DBSOURCE swissprot: locus OM1D_CHLTR, accession Q46409;
 class: standard.
 created: May 30, 2000.
 sequence updated: Nov 1, 1996.
 annotation updated: May 2, 2006.
 xrefs: X62918.1, CAA44701.1, AF063195.2, AAC31436.2, AE001273.1,
 AAC68276.1, H71484
 xrefs (non-sequence databases): PHCI-2DPAGE:Q46409,
 GenomeReviews:AE001273_GR, InterPro:IPR000604, Pfam:PF01308,
 PRINTS:PR01334
 KEYWORDS Complete proteome; Ion transport; Membrane; Outer membrane; Porin;
 Signal; Transmembrane; Transport.
 SOURCE *Chlamydia trachomatis*
 ORGANISM *Chlamydia trachomatis*
 Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 REFERENCE 1 (residues 1 to 393)
 AUTHORS Sayada, C., Denamur, E. and Elion, J.
 TITLE Complete sequence of the major outer membrane protein-encoding gene
 of *Chlamydia trachomatis* serovar Da
 JOURNAL Gene 120 (1), 129-130 (1992)
 PUBMED 1398119
 REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 STRAIN=D/B-120
 REFERENCE 2 (residues 1 to 393)
 AUTHORS Stothard, D.R., Boguslawski, G. and Jones, R.B.
 TITLE Phylogenetic analysis of the *Chlamydia trachomatis* major outer
 membrane protein and examination of potential pathogenic
 determinants
 JOURNAL Infect. Immun. 66 (8), 3618-3625 (1998)
 PUBMED 9673241
 REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 STRAIN=D/IU-71960
 REFERENCE 3 (residues 1 to 393)
 AUTHORS Stephens, R.S., Kalman, S., Lammel, C., Fan, J., Marathe, R.,
 Aravind, L., Mitchell, W., Olinger, L., Tatusov, R.L., Zhao, Q.,
 Koonin, E.V. and Davis, R.W.
 TITLE Genome sequence of an obligate intracellular pathogen of humans:
Chlamydia trachomatis
 JOURNAL Science 282 (5389), 754-759 (1998)
 PUBMED 9784136
 REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 STRAIN=D/UW-3/CX
 COMMENT On Sep 27, 2005 this sequence version replaced gi:7442973.
 [FUNCTION] Structural rigidity of the outer membrane of elementary
 bodies and porin forming, permitting diffusion of solutes through
 the intracellular reticulate body membrane.
 [SUBUNIT] Disulfide bond interactions within and between MOMP
 molecules and other components form high molecular-weight
 oligomers.
 [SUBCELLULAR LOCATION] Bacterial cell outer membrane; multi-pass
 membrane protein.
 [SIMILARITY] Belongs to the chlamydial OMP family.
 FEATURES
 source Location/Qualifiers
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 /db_xref="taxon:813"
 gene 1..393
 /gene="ompA"
 /locus_tag="CT_681"

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                                stephens momp
Protein      /note="synonym: omp1"
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              /gene="ompA"
              /locus_tag="CT_681"
              /product="Major outer membrane protein, serovar D
Region        precursor"
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              /locus_tag="CT_681"
              /region_name="Signal"
              /inference="non-experimental evidence, no additional
Region        details recorded"
              /note="By similarity."
              23..393
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              /locus_tag="CT_681"
              /region_name="Mature chain"
              /experiment="experimental evidence, no additional details
              recorded"
              /note="Major outer membrane protein, serovar D.
              /FTId=PRO_0000020147."

ORIGIN
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61 rvgyygdfvf drvlktdvnk efqmgakptt dtgnsaapst ltarenpayg rhmqdaemft
121 naacmalniw drfdvfctlg atsgylkgns asfnlvglfg dnengktvka esvpmnsfdq
181 svvelytdtt fawsvgaraa lwecgcatlg asfyaqskp kveelnvlcn aaftinkpk
241 gyvgkefpld ltagtdaatg tkdasidyhe wqaslalsyr lnmftpyigv kwsrasfdad
301 tiriaqpkas taifdtttln ptiagagdvk tgaegqlgdt mqivslqlnk mksrkscgia
361 vgttividak yavtvetrli deraahvnaq frf

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